

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clough, David W.
 - (B) REGISTRATION NUMBER: 36,107
 - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 180..1316
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGGCATTT GATCCCGCTG	120
CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGCGCCACA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu	227
1 5 10 15	
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys	275
20 25 30	
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp	323
35 40 45	
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys	371
50 55 60	
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe	419
65 70 75 80	
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu	467
85 90 95	
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser	515
100 105 110	
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val	563
115 120 125	
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly	611
130 135 140	
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu	659
145 150 155 160	
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp	707
165 170 175	
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn	755
180 185 190	

GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC 803
 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
 195 200 205

 TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC 851
 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
 210 215 220

 CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC 899
 Gln Lys Cys Ile Val Gln Thr Ser Trp Ser Gln Cys Ser Lys Ser
 225 230 235 240

 TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC 947
 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
 245 250 255

 CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA 995
 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
 260 265 270

 CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG 1043
 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
 275 280 285

 AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC 1091
 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
 290 295 300

 AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC 1139
 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
 305 310 315 320

 TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA 1187
 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
 325 330 335

 GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA 1235
 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
 340 345 350

 TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC 1283
 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
 355 360 365

 AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCT 1336
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
 370 375

 AGTGTGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGTGG GCGGAGGATG 1396

 AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAAGTGCC AAGGGGCTGA 1456

 TGTGGACGGA CAGCAGCGCA GCCG 1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
1 5 10 15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
100 105 110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
165 170 175

Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
180 185 190

Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
195 200 205

Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
210 215 220

Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
225 230 235 240

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
 245 250 255

 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
 260 265 270

 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
 275 280 285

 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
 290 295 300

 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
 305 310 315 320

 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
 325 330 335

 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
 340 345 350

 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
 355 360 365

 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 124..1266
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGCC	ACCGCGACAC	CGCGCCGCCA	CCCCGACCCC	GCTGCGCACG	GCCTGTCCGC	60
TGCACACCAG	CTTGTGGCG	TCTTCGTCGC	CGCGCTCGCC	CCGGGCTACT	CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT						168
Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu						
1	5		10		15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC						216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His						

	20	25	30	
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG				264
Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg				
35	40	45		
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC				312
Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp				
50	55	60		
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC				360
Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn				
65	70	75		
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA				408
Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser				
80	85	90	95	
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA				456
Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu				
100	105	110		
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC				504
Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala				
115	120	125		
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG				552
Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu				
130	135	140		
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG				600
Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu				
145	150	155		
GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG				648
Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln				
160	165	170	175	
GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG				696
Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu				
180	185	190		
TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG				744
Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu				
195	200	205		
AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT				792
Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro				
210	215	220		
TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC				840
Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys				
225	230	235		
TCA AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC				888
Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn				
240	245	250	255	

40053
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40053

CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro 260 265 270	936
TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser 275 280 285	984
AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys 290 295 300	1032
TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp 305 310 315	1080
GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe 320 325 330 335	1128
CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln 340 345 350	1176
TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe 355 360 365	1224
CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp 370 375 380	1266
TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT	1326
CAGAACATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA	1386
AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT	1418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu	
1 5 10 15	

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
100 105 110

Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
180 185 190

Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
195 200 205

Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
210 215 220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
225 230 235 240

Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
245 250 255

Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
260 265 270

Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
275 280 285

Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
290 295 300

Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
305 310 315 320

Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
325 330 335

Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
340 345 350

Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
355 360 365

Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC GACAACCCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCC 60
CTGTCCGAAT CCAGGCTCCA GCCGCGCCTC TCGTCGCCTC TGCACCCTGC TGTGCATCCT 120
CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCCTTGGTGC 180
TCCTCGCCCT CTGCACCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCAGTGCG 240
CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT 300
GCTGCCGCGT CTGCGCCAAG CAGCTGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC 360
CACACAAGGG CCTCTTCTGC GATTTGGCT CCCCCGCCAA CCGCAAGATT GGAGTGTGCA 420
CTGCCAAAGA TGGTGCACCC TGTGTCTTCG GTGGGTCGGT GTACCGCAGC GGTGAGTCCT 480
TCCAAAGCAG CTGCAAATAC CAATGCCACTT GCCTGGATGG GGCGTGGGC TGCCTGCC 540
TATGCAGCAT GGACGTGCGC CTGCCAGCC CTGACTGCC CTTCCCGAGA AGGGTCAAGC 600
TGCCTGGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG 660
GCCCTGCCCT AGCTGCCTAC CGACTGGAAG ACACATTGG CCCAGACCCA ACTATGATGC 720
GAGCCAAGT CCTGGTCCAG ACCACAGAGT GGAGCGCCTG TTCTAAGACC TGTGGAATGG 780
GCATCTCCAC CCGAGTTACC AATGACAATA CCTTCTGCAG ACTGGAGAAG CAGAGCCGCC 840
TCTGCATGGT CAGGCCCTGC GAAGCTGACC TGGAGGAAAA CATTAAGAAG GGCAAAAAGT 900

GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTGA GCTTCTGGC TGCACCAGTG 960
 TGAAGACATA CAGGGCTAAG TTCTCGGGGG TGTGCACAGA CGGCCGCTGC TGCACACCGC 1020
 ACAGAACAC CACTCTGCCA GTGGAGTTCA AATGCCCGA TGGCGAGATC ATGAAAAAGA 1080
 ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAAC TGCTGGGGAC AATGACATCT 1140
 TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG 1200
 ACACGAACTC ATTAGACTAT AACTTGAAC GAGTTGCATC TCATTTCTT CTGTAAAAAC 1260
 AATTACAGTA GCACATTAAT TTAAATCTGT GTTTTTAACT ACCGTGGGAG GAACTATCCC 1320
 ACCAAAGTGA GAACGTTATG TCATGCCAT ACAAGTAGTC TGTCAACCTC AGACACTGGT 1380
 TTCGAGACAG TTTACACTTG ACAGTTGTT ATTAGCGCAC AGTGCCAGAA CGCACACTGA 1440
 GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT 1500
 TATTTAAAAA GCAGCAGTGT GCCTACTTT TGGAGTGTAA CCGGGGAGGG AAATTATAGC 1560
 ATGCTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCCCTCAC TAGATGAGGC 1620
 TGAGTCCAGC TGTTCTTAA GAACAGCAGT TTCAGCCTCT GACCATTCTG ATTCCAGTGA 1680
 CACTTGTCAAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTG 1740
 CCTGTAACAA GCCAGATTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA 1800
 TATATTGTA CAGTTATCTA AGTTAATTAA AAGTCATTG TTTTGTTT AAGTGCTTT 1860
 GGGATTTAA ACTGATAGCC TCAAACCCA AACACCATAG GTAGGACACG AAGCTTATCT 1920
 GTGATTCAA ACAAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCA 1980
 AACAAACAAA TGCTGTGCAG GTGATAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA 2040
 AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTAT TAAGAAATGG CTGGCTCAGG 2100
 GTAAGGTCCG ATTCCCTACCA GGAAGTGCTT GCTGCTTCTT TGATTATGAC TGTTTGGGG 2160
 TGGGGGGCAG TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTGCA CCTTTCTAGT 2220
 TGAAAATAAA GTATATATAT ATTTTTATA TGAAAAAAA GGAATTC 2267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
1 5 10 15

Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
20 25 30

Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
35 40 45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
50 55 60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
65 70 75 80

Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
85 90 95

Lys Asp Gly Ala Pro Cys Val Phe Gly Ser Val Tyr Arg Ser Gly
100 105 110

Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
115 120 125

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
130 135 140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
145 150 155 160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
165 170 175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
180 185 190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
195 200 205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
210 215 220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
225 230 235 240

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
245 250 255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
260 265 270

Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
275 280 285

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu Phe
290 295 300

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys
305 310 315 320

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
325 330 335

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2075 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGGCGAC AGCCCCGAGA CGACAGCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA	120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCCTCCTC	180
GCCCTCTGCA GCCGGCCGGC CGTCGGCCAG AACTGCAGCG GGCGTGCAG GTGCCCGGAC	240
GAGCCGGCGC CGCGCTGCCG GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC	300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC	360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC	420
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACC GCAGCGGAGA GTCCCTCCAG	480
AGCAGCTGCA AGTACCAGTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC	540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCCCTCC CGAGGAGGGT CAAGCTGCC	600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCAAGG ACCAAACCGT GGTTGGGCCT	660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCAG ACCCAAACAT GATTAGAGCC	720
AACTGCCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC	780

TCCACCCGGG TTACCAATGA CAACGCCCTCC TGCAGGCTAG AGAACAGAG CCGCCTGTGC 840
 ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC 900
 CGTACTCCA AAATCTCCA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG 960
 ACATAACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA 1020
 ACCACCACCC TGCCGGTGGA GTTCAAGTGC CCTGACGGCG AGGTCAATGAA GAAGAACATG 1080
 ATGTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTGAA 1140
 TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT 1200
 AACTCATTAG ACTGGAACCT GAACTGATTAC ACATCTCATT TTTCCGTAAA AATGATTTC 1260
 GTAGCACAAAG TTATTTAAAT CTGTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA 1320
 AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT 1380
 TAAGACTTGA CAGTGGAACT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC 1440
 TTTAGGAGCA GTGGGAGGGT ACCGGCCCGG TTGAGTATCAT CAGATCGACT CTTATACGAG 1500
 TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT 1560
 GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTC 1620
 GTTGTTCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTGAA ATGACACTGT 1680
 TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA 1740
 ACAAGCCAGA TTTTTAAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA 1800
 TATATATATA TATGTACAGT TATCTAAGTT AATTAAAGT TGTTTGTGCC TTTTTATT 1860
 TGTTTTAAAT GCTTTGATAT TTCAATGTTA GCCTCAATT CTGAACACCA TAGGTAGAAT 1920
 GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG 1980
 ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGGCA 2040
 GGCTGATTTC TAGGTAGGAA ATGTGGTAGC TCACG 2075

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145 150 155 160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180 185 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225 230 235 240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Cys
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305 310 315 320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
340 345

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCC AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

**
* D E S C R I P T I O N *
* C O D E : 2 0 0 0 *
* P A T T E R N : 3 *
* P A T T E R N : 3 *

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
1 5 10 15

Cys Ser Lys Thr Gln
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys
1 5 10 15

Ile Pro Leu Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly
1 5 10 15

Thr Gly Ile Ser Thr Arg Val Thr
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
1 5 10 15

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln
1 5 10 15

Thr Arg Thr Val Lys
20